

## PUBLIC VERSION -- REDACTED

IN THE UNITED STATES DISTRICT COURT  
FOR THE DISTRICT OF DELAWARE

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NOVOZYMES A/S,		
Plaintiff,		C.A. No. 05-160-KAJ
v.		
GENENCOR INTERNATIONAL, INC. and		
ENZYME DEVELOPMENT CORPORATION,		
Defendants.		

### DECLARATION OF GREGORY K. LEFEBVRE

I, Gregory K. LeFebvre, do hereby declare as follows:

1. I make this declaration in support of the Motion of Novozymes A/S for a Preliminary Injunction. I have personal knowledge of the facts set forth herein and if called to testify, I could and would truthfully testify to them.
2. I am currently an employee of Novozymes of North America, Inc. ("Novozymes" may refer to either Novozymes A/S or to Novozymes of North America, Inc., as the case may be). My current job title is Senior Marketing Manager of Ethanol Industries, where I am responsible for global marketing of enzyme products and services to the ethanol industries. I have been an employee of Novozymes since 1984. During my employment at Novozymes I have held positions as Assistant Chemist, Chemist, Group Leader, Market Development Manager of the Foods Group, Regional Marketing Manager of Cereal Foods, Regional Marketing Manager of the Brewing and Juice Industries, and Regional Marketing Manager of the Starch and Fuel Ethanol Industries. In the course of my employment at Novozymes, I have been

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involved in and directed work in marketing and technical support activities in the above-mentioned markets..

3. My educational background includes a 1983 B.S. in Biochemistry from Sacred Heart University, Fairfield, Connecticut, and a 1998 M.B.A. from the University of Connecticut, Storrs, Connecticut.

4. Alpha-amylases are useful in a variety of commercial applications that involve the processing of starches -- especially in the fuel ethanol industry, where ethanol fuel is produced from starch crops such as corn, barley, and wheat. Alpha-amylase enzymes are used in this particular industry to liquefy and reduce viscosity of the starch feedstocks, thereby facilitating their processing in the manufacturing plant. In a subsequent step, another industrial enzyme, gluco-amylase (one of which is also made by Novozymes), is used to convert the liquefied starch into fermentable sugars (e.g., glucose). Yeast then converts the sugars into ethanol.

5. Novozymes produces and sells several enzyme products in the United States which are important to the fuel ethanol industry. Novozymes' Liquozyme® SC and Termamyl® are each alpha-amylase products which reduce starch viscosity by breaking complex starches into small molecules. Novozymes' Spirizyme® Fuel products are gluco-amylases which convert the less viscous, smaller liquefied starches to even smaller glucose molecules which yeast ferment into ethanol. Before Genencor introduced its infringing Spezyme® Ethyl alpha-amylase enzyme product in 2004, these Novozymes' enzyme products had gained wide-market acceptance. Novozymes also produces and sells its patented Termamyl SC alpha-amylase product to the food and beverage industry. It is used to break down starches into smaller sugars in this industry, as well

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6. Absent immediate injunctive relief to return to the *status quo*, Novozymes will suffer irreparable harm. In particular, the unabated marketing and sales of Genencor's infringing alpha-amylase enzyme product have already caused, and will likely continue to cause, (i) irreversible alteration of relevant market conditions to the significant detriment of Novozymes; (ii) Novozymes' significant loss of market share, goodwill, and customers, as well as the loss of its related convoyed sales of gluco-amylase enzyme products; and (iii) Novozymes' loss of a large annual supply agreement, expected to be awarded in just four months from now (in October 2005), covering a collective of domestic plants [REDACTED]  
[REDACTED], that will not reopen until October 2006. None of these losses, and certainly not the cumulative affect of the losses, can be adequately compensated by money damages.

7. Genencor is establishing itself as a supplier of a competing alpha-amylase enzyme only by infringing Novozymes' '031 patent. If Genencor is permitted to continue this activity, post-litigation market conditions will change so significantly that the market will not readily return to pre-infringement conditions. In addition, the longer that present Novozymes customers can purchase infringing alpha-amylase enzyme products from Genencor, the more difficult it will be for Novozymes to re-establish its pre-infringement market conditions once Genencor's product is permanently enjoined at the conclusion of this litigation.

8. Genencor's continued infringement will also detrimentally affect Novozymes' pre-infringement reputation.

9. In the absence of a preliminary injunction and return to the *status quo*, it is also likely that more customers will begin to use or switch to Genencor's "me-too" infringing product. If Genencor is permitted to sell its infringing enzyme until a permanent injunction is

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granted after a full trial, it will be very difficult to return the market to pre-infringement conditions where Novozymes enjoyed a good reputation as a reliable industrial enzyme supplier in general, and a reliable alpha-amylase industrial enzyme supplier in particular.

10. Requiring Genencor customers to switch to Novozymes' enzyme product after imposition of permanent injunctive relief will quite likely result in resentment towards Novozymes, because such a switch will likely impose additional costs to the customer. Because Genencor's enzymes are used in industrial processes that are developed, tested, and scaled-up before they are actually "qualified" by the customer for commercial use, the substitution of one supplier's enzyme for another's requires testing and adjusting of the process (different supplier's enzymes may differ to some degree in properties or strengths). Thus, an enzyme user must spend time and money testing and adjusting his process to accommodate a change in suppliers.

11. Enzyme users who purchase Genencor's infringing product will return to Novozymes' products (i) only if necessary, (ii) only with resentment and resistance, and (iii) only at real costs. The resulting damage to Novozymes' goodwill cannot be adequately compensated by an award of money damages at the conclusion of trial.

12. Novozymes has been forced [REDACTED]

[REDACTED] to compete with Genencor's infringing product. Novozymes remains under constant price pressure from its customers who have been offered the infringing Spezyme Ethyl alpha-amylase product. Damages resulting from this price erosion are incalculable because their effects could last for decades, especially where Novozymes' customers are resistant to any subsequent rise in the price of the alpha-amylase product.

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13. Price pressure from Genencor has translated into non-compensable lost market share where Novozymes' customers have opted to purchase the infringing Genencor product instead of the product offered by Novozymes.

14. Before Genencor entered the market in April 2004, Novozymes had about [REDACTED] percent (by sales) of the United States fuel ethanol alpha-amylase market. Since Genencor entered the market, the market share for Liquozyme SC [REDACTED]

[REDACTED] because of Genencor's infringing activities. This trend promises to worsen as long as Genencor's infringing Spezyme Ethyl alpha-amylase product remains on the market. This loss of market share and corresponding price erosion, translates into a significant, immeasurable, and non-compensable loss to Novozymes.

15. Novozymes' damages are further non-compensable because its lost customers and market share extend beyond the alpha-amylase market.

16. Commercial enzyme users, at times, purchase several different types of enzymes, rather than a single enzyme. Customers may also prefer to purchase their enzyme needs from as few suppliers as possible to concentrate their buying power and receive the best pricing, supply, and service.

17. It is common in the relevant market here that, when a customer shifts its purchases of one enzyme product from one supplier to another, the purchaser will also seek to shift its purchases of other enzyme products to that new supplier. [REDACTED]

[REDACTED], unless defendants' infringing activities are stopped immediately and the previous *status quo* is maintained.

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18. Because of Genencor's infringing sales of Spezyme® Ethyl, Novozymes has suffered a loss in market share, not just of its Liquozyme SC and Termamyl alpha-amylase enzyme products, but also for its convoyed gluco-amylase enzyme sales.

19. Both of Novozymes's alpha-amylase enzyme product lines, Liquozyme SC and Termamyl, were established product lines in the fuel ethanol and starch processing industries prior to the commencement of Genencor's infringing sales. Every day that Genencor is allowed to offer its infringing product, Novozymes suffers irreparable harm that undermines these established product lines.

20. I believe that Genencor will not suffer any significant undue hardship if preliminarily enjoined from infringing Novozymes' '031 patent. Genencor sells another alpha-amylase enzyme product (called Spezyme® Fred), and it sells many other enzyme products as well. If preliminarily enjoined, Genencor will still have other remaining non-infringing enzyme product lines to sell.

21. Novozymes is an international leader in the research, development, and marketing of commercial enzymes. In 1979, Novozymes opened a manufacturing facility in Franklinton, North Carolina. Since 1990, Novozymes has spent over \$150,000,000 on plant expansions at that facility. It is now the largest manufacturing plant for industrial enzymes in the United States.

22. Novozymes presently plans [REDACTED]. Its Franklinton facility includes a research laboratory and a pilot plant, where new enzymes and uses for enzymes are discovered and developed. Much of this research is directed at solving problems brought to Novozymes by customers.

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23. Novozymes has built a reputation through innovation and has protected its innovations through patents. If Novozymes could not protect its proprietary technology in the U.S. through patents, it would not have invested as heavily in its research or facilities in the U.S. and will not continue to invest in this manner.

24. Franklinton consists mainly of farms and small businesses. Novozymes is Franklinton's largest employer, and most of Franklinton's businesses depend in some part on Novozymes and its employees.

25. Genencor has begun to sell an infringing food grade Spezyme Ethyl product to the food and beverage industry outside of the United States, and has begun sampling it to this industry in the United States. I believe it is likely that Genencor will soon begin U.S. sales of its food grade infringing product. Novozymes presently sells its patented Termamyl SC alpha-amylase product to this industry. I believe further that Genencor's sales of Spezyme Ethyl to the U.S. food and beverage industry will cause irreparable harm to Novozymes in yet another segment of the commercial enzyme business.

26. There is a significant likelihood that, if Genencor's patent infringement is not preliminarily enjoined, Novozymes will likely continue to suffer irreversible and unfairly precipitated price reductions and loss of market share, not just for its Liquozymes SC alpha-amylase enzyme product, but also for its convoyed sales of related gluco-amylase enzyme products as well. These products are functionally related because Novozymes' gluco-amylase product is used in a subsequent process step to the use of Novozymes' alpha-amylase product in the making of ethanol.

27. The reduced demand caused by the attendant loss of all such sales could require Novozymes to reduce operations at its sole U.S. plant, based in Franklinton, North Carolina, that

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domestically produces its Liquozymes SC product, where Novozymes is the largest employer (about 400 jobs) and driver of the local economy.

28. Genencor remained on the market even after it learned that Novozymes' allowed patent application (which led to the '031 patent) would cover Genencor's alpha-amylase enzyme product upon issuance of the patent. This was so because on September 29, 2001 Novozymes voluntarily gave Genencor a copy of the allowed patent claims from the application in the hope that Genencor would see the fruitlessness of continuing to sell its product.

29. I am not aware of any critical public interest that would be injured by Novozymes' grant of the requested preliminary relief. However, the public interest of the people in Franklinton, North Carolina, may be adversely affected if the preliminary injunction is not granted. In particular, although the Franklinton plant makes both alpha-amylase and gluco-amylase enzyme products and only about █% of the plant is devoted solely to alpha-amylase production, the continued loss of Novozymes' business (and profits) for both product lines could adversely affect employment opportunities at the plant.

30. Further declarant saith not.

I declare under penalty of perjury under the laws of the United States of America that the foregoing is true and correct.

Dated: June 22, 2005 /s/

Gregory K. LeFebvre

**EXHIBIT E**



A GENUINE MERRIAM-WEBSTER

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parasitic • parenthesis 855

W abut \w\ biffen, F table \v\ further \v\ ash \v\ aise \v\ cat, east  
 vau, out \v\ ch\ chin, a bet, a benny \v\ go \v\ hit, \v\ ice \v\ job  
 \v\ sing \v\ go, \v\ law, \v\ on boy, \v\ on thin, \v\ on the, \v\ u, \v\ foot  
 \v\ yet, \v\ zhi vision \v\ z, \v\ e, \v\ ee, \v\ ie, \v\ ee. *(See Guide to Pronunciation)*

## 1304 Vanir • variocoupler

Vanir *Vánar* (3) n. pl. [ON]: a race of Norse gods who became united with the Aesir  
 vanish *Vánish* vb [ME *vánissh*, fr. MF *vánissier*, stem of *vánir*, fr. (assumed) VL *vánissare*, alter. of L *vanesse* to dissipate like vapor, vanish, fr. *et* + *vanesse* to vanish, fr. *vánus* empty] v. (14c) 1: a: to pass quickly from sight : DISAPPEAR b: to pass completely from existence 2: to assume the value zero ~ n: to cause to disappear — *Vanisher* n.

vanishing cream n (1922): a cosmetic preparation that is less oily than cold cream and is used chiefly as a foundation for face powder

vanishingly *Ver-e-shi-ly* adv (1870): so as to be almost nonexistent or invisible (the difference is ~ small)

vanishing point n (ca. 1797) 1: a point at which receding parallel lines seem to meet when represented in linear perspective 2: a point at which something disappears or ceases to exist

vanity *Vánit* n. pl. ties [ME *vante*, fr. OF *vante*, fr. L *vanius*, *vanius* quality of being empty or vain, fr. *vana* empty, vain — *inane* of WANE] (13c) 1: something that is vain, empty, or vainglorious 2: the quality or fact of being vain 3: inflated pride in oneself or one's appearance CONCEIT 4: a fashionable trifle or knickknack 5: a: **COM-FACTA** b: a small case or handbag for toilet articles used by women 6: DRESSING TABLE

vanity fair n. often cap. V&F [Vanity Fair], a fair held in the frivolous town of Vanity in *Pilgrim's Progress* (1678) by John Bunyan; (1816): a scene or place characterized by frivolity and ostentation

vanity plate n (1966): a license plate bearing letters or numbers designated by the owner of the vehicle

vanity press n (1950): a publishing house that publishes books at the author's expense — called also *vanity publisher*

van-nee *Ván-e-né* n (1927): a person who owns a usu. customized van vanpool *Ván-pool* n [van + car pool] (ca. 1974): an arrangement by which a group of people commute to work in a van — *vanpooling* n

vanquish *Van-kwísh* v. *vánish* n [ME *venguissien* fr. MF *vaquissir*, prefer of *vétre* to conquer, fr. L *vincere* — more at VICTOR] (14c) 1: to overcome in battle : subdue completely 2: to defeat in a conflict or contest 3: to gain mastery over (an emotion, passion, or temptation) SYN see CONQUER 4: vanquishable *Van-kwísh-á-bíl* adj — *Vanquisher* n

van-tile *Ván-tíl* n. (ME, fr. AF, fr. MF *vau-tile* — more at ADVANTAGE) (14c) 1: *advantage*; BENEFIT, GAIN 2: superiority in a contest 3: a position giving a strategic advantage, commanding perspective, or comprehensive view 4: ADVANTAGE — to the vantage obs: in addition

vantage point (1865): a position or standpoint from which something is viewed or considered esp: POINT OF VIEW

vanguard *Ván-gárd* adj (1810): located in the vanguard : ADVANCED, FORWARD — *vanguard* n

va-pid *Váp-id* adj [L *vapidus* hot tasting, akin to L *vappa*, *vapid*, *vapid*, *vapid* wine and probe to L *vapor* steam] (ca. 1656): lacking liveliness, tang, briskness, or force; FLAT, UNINTERESTING SYN see INSPID — *Vapidly* adv — *Vapid-ness* n

va-pid-ity *Váp-id-íté*, *Váp-id-ñé* n. pl. ties (ca. 1721) 1: the quality or state of being VAPID 2: something VAPID

va-por *Váp-or* n [ME *vapour*, fr. MF *vapeur*, fr. L *vapor* steam, vapor] (14c) 1: diffused matter (as smoke or fog) suspended floating in the air and impairing its transparency 2: a substance in the gaseous state as distinguished from the liquid or solid state 3: a substance (as gasoline, alcohol, mercury, or benzoin) vaporized for industrial, therapeutic, or military uses; also: a mixture (as the explosive mixture in an internal-combustion engine) of such a vapor with air 3 a: something unsubstantial or transitory: PHANTASM b: a foolish or fanciful idea 4 pl. a: *archaic*: exhalations of bodily organs (as the stomach) held to affect the physical or mental condition b: a depressed, or hysterical nervous condition

vapor wa-pored; va-poring *Váp-ör-ing* (15c) 1: a: to rise or pass off in vapor b: to emit vapor 2: to indulge in bragging, blustering, or idle talk — *vapored*, *vapored* n

vapor barrier n (ca. 1941): a layer of material (as roofing paper or polyethylene film) used to retard or prevent the absorption of moisture into a construction (as a wall or floor)

va-po-rot-e *Váp-o-rét-e* n. pl. -ret-és *Ver-e-ád-a*-ret-és [L, dim. of *vapore* steamboat, fr. *Vapeur*, fr. *bateau* a *vapeur* steamboat] (1949) a: a motorboat serving as a canal bus in Venice, Italy

va-poring *Váp-ör-ing* n (1610): the act or speech of one that vapors; specif: an idle, extravagant, or high-flown expression or speech — usu. used in pl.

vapor-ize *Váp-ör-íz*, Brit var of VAPORIZE

vapor-isti *Váp-ör-íst* adj (ca. 1644) 1: resembling or suggestive of vapor 2: given to fits of the vapors — *vaporousness* n

vapor-ize *Váp-ör-íz* vb -ized; -iz-ing v. (1514) 1: to convert (as by the application of heat or by spraying) into vapor 2: to cause to become VAPORIZED ~ vt 1: to become VAPORIZED 2: VAPORIZE — *vaporizable* *Váp-ör-íz-á-bíl* adj — *vaporizer* *Váp-ör-íz-ör* n (ca. 1846) 1: one that vaporizes; as: a: ATOMIZER b: an apparatus for vaporizing a heavy oil (as petroleum) for the explosive charge of an internal-combustion engine; also: a simple form of carburetor c: a device for converting water or a medicated liquid into a vapor for inhalation

vapor lock n (ca. 1926): partial or complete interruption of flow of a fluid (as fuel in an internal-combustion engine) caused by the formation of bubbles of vapor in the leading system

vaporous *Váp-ör-ús* adj (1527) 1: consisting or characteristic of vapor 2: producing vapors: VOLATILE 3: containing or obscured by vapors: MISTY 4: a: ETHEREAL, UNSUBSTANTIAL b: consisting of or indulging in vapors — *vaporously* adv — *vaporousness* n

vapor pressure n (ca. 1900): the pressure exerted by a vapor that is in equilibrium with its solid or liquid form — called also *vapor tension*

vapor trail n (1943): CONTRAIL

vapor *Váp-or* n. pl. -ors [Sp — more at BUCKAROO] (1511)

va-pour *Váp-ör* chiefly Brit var of VAPOR

va-por-e-ro *Váp-ör-é-ro* n [Sp & Pg, lit., pole, fr. L, forked pole, fr. fem. of *varus*, bent, crooked — more at PREVARICATE] (1604) 1: any of various Spanish, Portuguese, and Latin-American units of length equal to be-

tween 31 and 34 inches (79 and 86 centimeters) 2: a Texas unit of length equal to 31.33 inches (84.66 centimeters)

var-: or var- comb form [L *varus* — more at VARIUS] : varied: diverse (variant) *Varicoupler*

varia *Ver-e-á*, *Var-e-á* n pl. of *varius* various (1926)

varia-: **MISCELLANY** esp: a literary miscellany

variable *Ver-e-á-bol*, *Var-e-á-bol* *Ver-e-á-ble*, *Var-e-á-ble* adj [ME, fr. L *variabilis*, fr. *varire* to vary] (14c) 1: a: able or apt to vary; subject to variation or changes (~ winds) (~ costs) b: **FICKLE, INCONSTANT** 2: characterized by variations 3: having the characteristics of a variable 4: not true to type: ABERRANT — used of a biological group or character 5: **variability** *Ver-e-á-bil-i-té*, *Var-e-á-bil-i-té* n — **variableness** *Ver-e-á-bil-i-té*, *Var-e-á-bil-i-té* n (1816) 1: a: a quantity that may assume any one of a set of values b: a symbol representing a variable 2: something that is variable 3: **VARIABLE STAR**

variable rate mortgage (1975): a periodically renegotiable mortgage that has an interest rate indexed to the cost of funds to the lender

variable star n (1783): a star whose brightness changes usu. in more or less regular periods

variance *Ver-e-á-nans* n. *Var-e-á-nans* [ME *variaunce*, fr. MF, fr. L *variancia*, fr. *varians* pp. of *varire* to vary] (14c) 1: the fact, quality, or state of being variable or variant: DIFFERENCE, VARIATION (yearly ~ in crops) 2: the fact or state of being in disagreement: DISSENSION, DISPUTE 3: a disagreement between two parts of the same legal proceeding that must be consonant 4: a license to do some act contrary to the usual rule (a zoning ~) 5: the square of the standard deviation SYN see DISCORD — at variance: not in harmony or agreement

variant *Ver-e-á-ant*, *Var-e-á-ant* *Ver-e-á-ble*, *Var-e-á-ble* adj: VARIABLE 2: manifesting variety, deviation, or disagreement 3: varying usu. slightly from the standard form (~ readings)

variant n (1848): one of two or more persons or things exhibiting usu. slight differences: as: a: one that exhibits variation from a type or norm b: one of two or more different spellings (as *labor* and *labour*) or pronunciations (as of *economics* *ék-ən-ómē* or *ék-ə-nómē*) of the same word c: one of two or more words (as *geographic* and *geographical*) or word elements (as *mono-* and *mono-*) or essentially the same meaning differing only in the presence or absence of an affix

variate *Ver-e-á-té*, *Var-e-á-té* n (1899): RANDOM VARIABLE

variation *Ver-e-á-shon*, *Var-e-á-shon* n [ME *variations*, fr. MF, fr. L *variations*] (14c) 1: a: the act or process of varying: the state or fact of being varied b: an instance of varying c: the extent to which or the range in which a thing varies 2: DECIMATION 6 3: a change in the mean motion or mean orbit of a celestial body 4: a: a change of algebraic sign between successive terms of a sequence b: a measure of the change in data: a variable, or a function 5: the repetition of a musical theme with modifications in rhythm, tune, harmony, or key 6: a: divergence in qualities of an organism or biotype from those typical or usual to its group b: something (as an individual or group) that exhibits variation 7: a: a solo dance in classic ballet b: a repetition in modern ballet of a movement sequence with changes — *variational* *Ver-e-á-shon-ál*, *Var-e-á-shon-ál* adj — *variationally* *Ver-e-á-ble* adj

vari-colla *Var-e-á-ko-lá* n [NL, irreg. dim. of *vario*] (ca. 1771)

vari-co-cole *Var-e-á-ko-kó-lé* n [NL, fr. L *varic*, *varix* + *-o* + *-cole*] (1716): a varicose enlargement of the veins of the spermatic cord

vari-col-ored *Ver-e-á-kó-lárd*, *Var-e-á-kó-lárd* adj (1665): having various colors

vari-egated *Ver-e-á-é-gá-té* ~ nuptial plumage of a bird; also: of various colors

vari-ose *Var-e-á-óz* adj [L *varicosus* full of dilated veins, fr. *varic*, *varix* dilated vein, akin to L *varus* stretched, bent, awry] (1730) 1: of, relating to, or exhibiting varices (~ in mollusks) 2: also *vari-cosed* *Ver-e-á-kóz*, *Var-e-á-kóz* adj: abnormally swollen or dilated (~ veins)

vari-osity *Var-e-á-óz-i-té*, *Var-e-á-óz-i-té* n (1842) 1: the quality or state of being abnormally or markedly swollen or dilated 2: **VARIX**

varied *Ver-e-á-íd*, *Var-e-á-íd* adj (1585) 1: VARIOUS, DIVERSE 2: **VARIATED** — *variedly* adv

varie-gate *Ver-e-á-é-gá-té*, *Var-e-á-é-gá-té* adj, *Ver-e-á-é-gá-té*, *Var-e-á-é-gá-té* v. *Ver-e-á-é-gá-té*, *Var-e-á-é-gá-té* v. *Ver-e-á-é-gá-té* pp. *Ver-e-á-é-gá-té* [L *variegare* pp. of *variegare*, fr. *varius* various + *-egare* (akin to L *egere* to drive) — more at AGENT] (1653) 1: to diversify in external appearance esp: with different colors: DAPPLE 2: to enliven or give interest to by means of variety — *variegator* *Ver-e-á-é-gá-tör* n

varie-gated *Ver-e-á-é-gá-té* adj (1661) 1: having discrete markings of different colors (~ leaves) 2: **VARIED**

variegated cutworm n (1922): a widespread nocturnal moth (*Peridroma saucia*) whose larva is destructive to crops

variegation *Ver-e-á-é-gá-shon*, *Var-e-á-é-gá-shon* n (1646) 1: the act of variegating: the state of being variegated; esp: diversity of colors

vari-er *Ver-e-á-ér*, *Var-e-á-ér* adj (1860) 1: one that varies

vari-etal *Ver-e-á-tál*, *Var-e-á-tál* adj (1866) 1: of, relating to, or characterized by variety (~ name); also: being a variety in distinction from an individual or species

varietal n (1950): a wine bearing the name of the principal grape from which it is made

vari-ety *Ver-e-á-té*, *Var-e-á-té* n pl. ties [MF or L, MF *variété*, fr. L *varietas* fr. *varius* various] (1548) 1: the quality or state of having different forms or types: MULTIFARIOUSNESS 2: a number or collection of different things esp: of a particular class: ASSORTMENT 3: a: something differing from others of the same general kind: SORT b: any of various groups of plants or animals ranking below a species: SUBSPECIES 4: VARIETY SHOW

variety meat n (ca. 1945) 1: an edible part (as the liver or tongue) of a slaughtered animal other than skeletal muscle

variety show n (1882): a theatrical entertainment of successive separate performances (as of songs, dances, skits, acrobatic feats, and trained animal acts)

variety-store n (ca. 1768): a retail store that carries a large variety of merchandise esp: of low-unit value

vario- — see *ARI*

vario-coupler *Ver-e-á-kó-pú-lár*, *Var-e-á-kó-pú-lár* n (ca. 1922): an inductive coupler the mutual inductance of which is adjustable by moving one coil with respect to the other

**EXHIBIT F**

IN THE UNITED STATES DISTRICT COURT  
FOR THE DISTRICT OF DELAWARE

NOVOZYMES A/S,

Plaintiff

C.A. No. 05-160-KAJ

v.

GENENCOR INTERNATIONAL, INC., and  
ENZYME DEVELOPMENT CORPORATION

Defendants

DECLARATION OF CHRISTIAN ISAK JØRGENSEN

I, Christian Isak Jørgensen, do hereby declare as follows:

1. I am a citizen of Denmark and am more than twenty-one (21) years of age.
2. I am a protein chemist in the Department of Protein Technology at Novozymes A/S ("Novozymes") in Bagsværd, Denmark. In that capacity, I am responsible for the sequencing and amino acid analysis of different proteins. I have been an employee at Novozymes since 2001.
3. In 1999, I received a Doctorate ("Ph.D.") degree in Molecular Biology from the University of Southern Denmark in Odense, Denmark. From 1999 until 2001, before I began working at Novozymes, I worked as a Research Scientist in the Department of Biochemistry and Molecular Biology at the University of Southern Denmark. Details of my education and professional experience are set forth in my *Curriculum Vitae*, which is submitted as Exhibit 1 along with this Declaration.

**I. BACKGROUND**

4. I understand that this Declaration is being submitted in support of a law suit between Novozymes A/S ("Novozymes"), and the parties Genencor International, Inc. ("Genencor") and Enzyme Development Corporation ("EDC"). In particular, I understand that Genencor and EDC have been accused of making and selling a product in the United States, called Spezyme Ethyl, that infringes a patent owned by Novozymes.

5. I have been given and have reviewed a document entitled "Spezyme Ethyl DNA Sequence", which is attached hereto at Exhibit 2. This document shows a nucleotide sequence which I understand to be the nucleotide sequence determined by Novozymes for DNA from a sample of the Spezyme Ethyl product that was sold in the United States. This document also shows an amino acid sequence, which I understand to be the amino acid sequence that is encoded by that DNA.

6. I have also been given what I understand to be samples of Genencor and EDC's Spezyme Ethyl product that were sold in the United States. These Spezyme Ethyl samples have been analyzed by me or by others working under my supervision and control to determine whether they contain the protein encoded by the DNA sequence at Exh. 2. From that analysis, I have found that Spezyme Ethyl does contain a protein encoded by that DNA sequence. The protein I analyzed from Spezyme Ethyl has the sequence of amino acid residues 30-513 of the protein sequence in Exh. 2. The complete amino acid sequence I have determined for that protein is shown at Exh. 3 of this Declaration.

7. I, or others working under my supervision and control, have also analyzed a protein expressed by a gene that encodes an alpha-amylase protein from a natural isolate of *Bacillus stearothermophilus*. This natural isolate is publicly available from the American Type

Culture Collection ("ATCC") and has been given the accession number ATCC 31,195. For convenience, therefore, the alpha-amylase from this isolate is referred to as the "ATCC 31,195 alpha-amylase".

8. The ATCC 31,195 alpha-amylase gene has been previously cloned, and its nucleotide sequence is available from the GenBank Database (Accession No. AF032864). A copy of that GeneBank entry, which includes the ATCC 31,195 alpha-amylase gene sequence, is attached to this Declaration at Exhibit 4. The sequence contains an open reading frame encoding an amino acid sequence that is also available from GenBank (Accession No. AAB86961), and is attached hereto at Exhibit 5.<sup>1</sup>

9. From my analysis, I have found that the protein expressed by the ATCC 31,195 alpha-amylase gene has the sequence of residues 35-523 of the protein sequence at Exh. 5. The complete sequence I have determined for that alpha-amylase is shown at Exhibit 6 of this Declaration.

10. The details of these analyses, and of the results obtained, are set forth *infra* in this Declaration.

## II. PROTEIN ANALYSIS OF SPEZYME ETHYL

11. This section of my Declaration describes experiments that were performed by me, or by others working under my supervision and control, to analyze protein in samples of the Spezyme Ethyl product that was sold in the United States. As explained above, I have found

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<sup>1</sup> The attached GenBank entries (Exhibits 4-5) indicate that the microorganism species is *Geobacillus stearothermophilus*. This is because the accepted name for this species of bacteria (i.e., for *Bacillus stearothermophilus*) has changed. The species is now known as *Geobacillus stearothermophilus*.

from these experiments that the Spezyme Ethyl samples contain a protein having the amino acid sequence set forth in Exhibit 3 of this Declaration.

*A. SDS-PAGE Analysis of Spezyme Ethyl*

12. In a first analysis, the protein components of the Spezyme Ethyl samples were separated by SDS-PAGE. Each of the samples was diluted twenty-fold with deionized water, followed by precipitation with trichloroacetic acid ("TCA"). The samples were resuspended in SDS-PAGE loading buffer containing 20 mM Tris-HCl pH 6.8, 2% SDS (w/v), 20% glycerol, 0.008% Bromophenol Blue ("BPB") (w/v), and 0.1 M diothiothreitol ("DTT"). The samples were incubated in the loading buffer for four minutes at 95 °C, and then loaded onto a standard, precast 4-20% SDS polyacrylamide gel for electrophoresis.

13. Following electrophoresis, the gel was incubated for five minutes in a standard blotting solution consisting of 10 mM 3-(cyclohexylamino)-1-propanesulfonic acid (CAPS), pH 11, and 6% methanol.

14. A ProBlott membrane from Applied Biosystems was used for electroblotting of the gel. The ProBlott membrane was soaked for one minute in pure methanol, and then placed in the blotting solution for five minutes. Electroblotting of the gel was carried out in a Semi Dry Blotter II apparatus from KemEnTec.

15. Following electroblotting, the ProBlott membranes were stained for 1 minute in 0.1% (w/v) Coomassie Brilliant Blue R-250 dissolved in a solution of 60% methanol, 1% acetic acid, and 39% distilled water. The ProBlott membranes were then incubated in 40% aqueous methanol for five minutes, followed by rinsing in deionized water. Finally, the ProBlott membrane was air dried.

16. For each sample a main protein band was identified on the ProBlott membrane that migrated at approximately 55 kDa. This protein was recovered from the SDS-PAGE for further analysis.

***B. N-Terminal Sequencing of the Spezyme Ethyl Protein***

17. The amino acid sequence of the protein recovered by SDS-PAGE was analyzed by N-terminal sequencing. For each sample a piece consisting of the main protein band at 55 kDa was cut out of the ProBlott membrane, and placed in the blotting cartridge of a Procise Protein Sequencer from Applied Biosystems.

18. N-terminal sequencing was carried out according to the manufacturer's instructions, using the method run file for PVDF membrane samples (pulsed liquid PVDF). The N-terminal amino acid sequence was determined from resulting chromatograms by comparing the retention time of the peaks in the chromatograms to retention times of PTH-amino-acids in a standard chromatogram. In addition, amino acid yields were determined by comparing the peak area to the corresponding standard peak area.

19. The protein recovered from the first sample of Spezyme Ethyl was thus found to have the following N-terminal sequence:

AAPFNGTMMQYFEWYLPDDGTLWTK.

20. Two N-terminal amino acid sequences were observed upon analysis of sequencing chromatograms obtained during N-terminal sequencing of protein recovered from the second sample of Spezyme Ethyl. The first sequence, which had the strongest intensity in the sequencing chromatograms, was identical to the N-terminal sequence found for the first sample.

21. The second N-terminal sequence detected in sequencing chromatograms of the second sample was as follows:

ANLNGTLMQYFEWY.

This second sequence had a much lower intensity (~10%) in the sequencing chromatograms compared to the first sequence, and is identical to the N-terminal amino acid sequence of a known *Bacillus licheniformis* alpha-amylase. This second sequence is not encoded by the DNA sequence encoding the Spezyme Ethyl protein. In my opinion, therefore, this second sequence is from a contaminant alpha-amylase which is endogenously expressed by the *Bacillus licheniformis* host cells used to recombinantly express the Spezyme Ethyl protein.

22. From this analysis, I find that the protein recovered from Spezyme Ethyl samples has the N-terminal sequence:

AAPFNGTMMQYFEWYLPDDGTLWTK.

This is identical to the sequence of amino acid residues 30 to 54 of the protein sequence at Exh. 2. This finding indicates that, during its expression by the host cell, the protein encoded by the DNA at Exh. 2 loses a secretion signal consisting of the first 29 amino acid residues encoded by that DNA.

**C. Molecular Weight Analysis of the Spezyme Ethyl Protein**

23. I have calculated the molecular weight of a protein having the amino acid sequence set forth in Exh. 2, but without the secretion signal sequence of the first 29 amino acids. That is to say, I have calculated the molecular weight of a protein having the sequence of residues 30-542 in the amino acid sequence set forth in Exh. 2. The average molecular weight of this protein, calculated using the program GPMAW version 6.2 from Lighthouse Data, is 58,535.56 Da.

24. I, or others working under my supervision and control, have also analyzed the Spezyme Ethyl protein by mass spectroscopy ("MS"), and thereby measured its average molecular weight.

25. For this analysis, 20 ml aliquots from the Spezyme Ethyl samples were dialyzed overnight at 5 °C, and against 20 liters of buffer containing 5 mM Tris-HCl pH 9.5 and 2 mM CaCl<sub>2</sub>. The dialyzed samples were filtered through a 0.45 µm filter to remove any precipitated material that may have been present, and applied to a Q-Sepharose FF column (26 x 120 mm) from Amersham Bioscience that had been equilibrated in 5 mM Tris-HCl pH 9.5 ("buffer A"). After application of protein sample, the column was washed with 10 column volumes of buffer A to remove unbound protein. Bound protein was eluted off of the column using a gradient of zero to 1 M NaCl in buffer A over 10 column volumes. Protein containing fractions were identified by their high absorbance of UV-light at 280 nm ("A<sub>280</sub>") as they eluted off the column. Fractions with a high A<sub>280</sub> value were analyzed by SDS-PAGE, to confirm that they contained the 55 kD protein component. Fractions containing that protein were then combined, and desalting by reverse-phase chromatography with a C4 reverse-phase column from Millipore.

26. The resulting samples of purified protein were analyzed using an online QTof™ tandem mass spectrometer from Micromass/Waters for exact mass measurements. Mass peaks at 55,129 Da appeared in both samples. This measured molecular weight is lower than the predicted molecular weight of 58,535.56 Da.

27. I, or others working under my supervision and control, also calculated the molecular weight of the protein having the amino acid sequence of residues 30-513 of the protein sequence at Exh. 2. I found that this protein has a calculated average molecular weight

55,129.60 Da. This calculated molecular weight is in accord with the measured average molecular weight of the protein from Spezyme Ethyl.

**D. Digestion of the Spezyme Ethyl Protein**

28. The protein component purified from the Spezyme Ethyl samples was further analyzed by digestion with cyanogen bromide (CNBr), in order to verify its determined amino acid sequence. CNBr cleaves peptide bonds at the carboxylic site of methionine residues. Hence, by treating a protein with CNBr under suitable conditions, the protein can be broken down or "digested" into smaller peptide fragments that end in methionine ("M").

29. Treatment of a protein having the amino acid sequence at Exh. 2 with CNBr will produce a peptide fragment with a calculated monoisotopic molecular weight of 8,660.47 Da molecular weight and having the amino acid sequence:

YVGKQHAGKVFYDLTGNRSDTVТИNSDGWGEFKVNGGSVSVWVPRKTTVSTIARPITT  
RPWTGEFVRWTEPRLVAWP.

However, if the protein's C-terminus ends at amino acid 513 of the sequence in Exh. 2, then this fragment will not be present. Instead, CNBr digestion of the protein will produce a peptide fragment with a calculated monoisotopic molecular weight of 5,256.64 Da, and having the amino acid sequence:

YVGKQHAGKVFYDLTGNRSDTVТИNSDGWGEFKVNGGSVSVWVPRKTT.

30. Purified protein from each of the Spezyme Ethyl samples was buffer exchanged to 0.1 M HCl by a Microcon YM-10 filter device from Millipore. One crystal of CNBr was added to each sample, and the samples were incubated for four hours at 37 °C. 0.5 µl aliquots from each protein sample were spotted directly to a MALDI-TOF target plate, to which 0.5 µl of CHCA matrix was then added, mixed, and allowed to dry. MALDI-TOF analysis of the samples

were done using a Voyager DE-PRO workstation from Applied Biosystems for exact mass measurements.

31. No protein fragments were identified that had a molecular weight of 8,660.47 Da. However, a protein fragment was detected that had a measured monoisotopic molecular weight of 5,256.3 Da. This fragment was collected, and the sequence of its first twelve amino acid residues was determined by N-terminal sequencing.

32. BioBrene Plus pretreated filters were prepared for N-terminal sequencing by adding 15  $\mu$ l of the BioBrene Plus solution (Applied Biosystems) to the filter, and cleaned by running four cycles of the Filter Precycle programme on a Procise Protein Sequencer (also from Applied Biosystems). The collected peptide fragments were then sequenced by adding 15  $\mu$ l of the collected samples to the pretreated BioBrene Plus filters. The filters were then loaded onto the Protein Sequencer, and sequenced using the Pulsed liquid method.

33. From this analysis, the sequence of the first twelve amino acid residues in the 5,256.3 Da fragment was determined to be: YVGKQHAGKVFY. This sequence confirms that the C-terminal digestion fragment had been isolated.

34. The results from this analysis confirm that the protein expressed by the DNA sequence at Exh. 2 ends at amino acid residue 513 of the protein sequence at Exh 2.

### **III. PROTEIN ANALYSIS OF THE ATCC 31,195 ALPHA-AMYLASE**

35. This section of my Declaration describes experiments that were performed by me, or by others working under my supervision and control, to analyze the protein expressed by the ATCC 31,195 alpha-amylase gene whose sequence is set forth at Exhibit 4. As explained above, I have found from these experiments that the alpha-amylase protein expressed by this gene has the amino acid sequence set forth at Exhibit 6 of this Declaration.

**A. N-Terminal Sequencing of the ATCC 31,195 Alpha-Amylase**

36. Samples of recombinant protein obtained by expressing the ATCC 31,195 alpha-amylase gene in *Bacillus subtilis* were analyzed by N-terminal sequencing, following the procedure described, *supra*, for N-terminal sequencing of protein in the Spezyme Ethyl samples.

37. Samples of the recombinant alpha-amylase protein were found to have the following N-terminal sequence: AAPFNGTMMQYFEWYLPDDGTLWTK. This is identical to the sequence of amino acid residues 35-59 of the protein sequence at Exh. 5. This finding confirms that the protein expressed by the ATCC alpha-amylase gene loses the secretion signal sequence of the first 34 amino acids.

**B. Molecular Weight Analysis of the ATCC 31,195 Alpha-Amylase**

38. I have calculated the molecular weight of a protein having the amino acid sequence set forth in Exh. 5 after the secretion sequence on its N-terminus has been removed. That is to say, I have calculated the molecular weight of a protein having the sequence of residues 35-549 in the amino acid sequence set forth in Exh. 5. The average molecular weight of this protein, calculated using the program GPMAW version 6.2 from Lighthouse Data, is 58,748.80 Da.

39. I, or others working under my supervision and control, have also analyzed the recombinant alpha-amylase expressed by the ATCC 31,195 alpha-amylase gene, using mass spectroscopy ("MS"). This analysis was performed as described, *supra*, for the Spezyme Ethyl protein. From this analysis, the recombinant ATCC 31,195 alpha-amylase was found to have an average molecular weight of 55,629 Da. This is lower than the calculated average molecular weight of 58,748.80 Da.

40. I, or others working under my supervision and control, also calculated the molecular weight of the protein having the amino acid sequence of residues 35-523 of the full length sequence encoded by the ATCC 31,195 alpha-amylase gene (*i.e.*, the protein sequence at Exh. 5). I found that this protein has a calculated average molecular weight of 55,630.17 Da. This calculated molecular weight is in accord with the measured average molecular weight of the recombinant ATCC 31,195 alpha-amylase protein.

**C. Digestion of the ATCC 31,195 Alpha-Amylase**

41. The recombinant alpha-amylase expressed by the ATCC 31,195 alpha-amylase gene was further analyzed by digestion with cyanogen bromide (CNBr).

42. Treatment of a protein having the amino acid sequence at Exh. 5 with CNBr will produce a peptide fragment with a calculated monoisotopic molecular weight of 8,660.47 Da, and having the amino acid sequence:

YVGKQHAGKVFYDLTGNRSDTVТИNSDGWGEFKVNGGSVSVWVPRKTTVSTIARPITT  
RPWTGEFVRWTEPRLVAWP.

However, if the protein's C-terminus ends at amino acid 523 of that sequence, then this fragment will not be present. Instead, CNBr digestion of the protein will produce a peptide fragment with a calculated monoisotopic molecular weight of 5,543.9 Da and having the amino acid sequence:

YVGKQHAGKVFYDLTGNRSDTVТИNSDGWGEFKVNGGSVSVWVPRKTTVST.

43. Samples of recombinant protein obtained by expressing the ATCC 31,195 alpha-amylase gene in *Bacillus subtilis* host cells were digested with CNBr; and the resulting fragments analyzed by MALDI-TOF mass spectrometry and N-terminal sequencing as described, *supra*, for CNBr digestion and analysis of the Spezyme Ethyl samples.

44. No protein fragments were identified that had a molecular weight of 8,660.47 Da. However, a protein fragment was obtained that had a measured monoisotopic molecular weight of 5,543.9 Da. The sequence of the first twelve amino acid residues in this fragment was determined by N-terminal sequencing, as described *supra* for Spezyme Ethyl, and found to be: YVGKQHAGKVFY. This sequence confirms that the C-terminal digestion fragment had been isolated.

45. The results from this analysis confirm that the protein expressed by the ATCC 31,195 alpha-amylase gene at Exh. 4 ends at amino acid residue 523 of the protein sequence at Exh. 5.

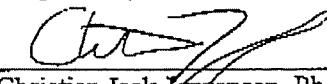
#### IV. CONCLUSION

46. From the foregoing analysis, I find that Spezyme Ethyl contains a protein of 484 amino acids having the amino acid sequence that is set forth in Exhibit 3 of this Declaration. I also find that the alpha-amylase protein expressed by the ATCC 31,195 alpha-amylase gene (Exh. 4) is a protein of 489 amino acids and having the amino acid sequence set forth in Exhibit 6 of this Declaration.

47. I declare under penalty of perjury pursuant to the laws of the United States of America that the foregoing statements are true and correct.

Respectfully submitted,

Dated: JUNE 16, 2005

  
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Christian Isak Jørgensen, Ph.D.

Attachments:

Exhibit 1: *Curriculum Vitae* of Christian Isak Jørgensen;

Exhibit 2: Spezyme Ethyl DNA Sequence;

Exhibit 3: Spezyme Ethyl Amino Acid Sequence;

Exhibit 4: GenBank Accession No. AF032864;

Exhibit 5: GenBank Accession NO. AAB86961; and

Exhibit 6: ATCC 31,195 alpha-amylase amino acid sequence.